

CRF Errors Corrected by the STIC Systems Branch

END P5/10

Serial Number: 101018, 311A **ENTERED**

CRF Processing Date: 6/11/2002
 Edited by: [Signature]
 Verified by: [Signature] (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. **DO NOT** send a copy of this form.

3/1/95



PCT10

RAW SEQUENCE LISTING

DATE: 06/11/2002

PATENT APPLICATION: US/10/018,311A

TIME: 19:42:00

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\06112002\J018311A.raw

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3 <110> APPLICANT: MIYATA, Toshio
4      KUROKAWA, Kiyoshi
6 <120> TITLE OF INVENTION: Meg-3 protein
8 <130> FILE REFERENCE: 2605/101
10 <140> CURRENT APPLICATION NUMBER: 10/018,311A
C--> 11 <141> CURRENT FILING DATE: 2002-04-19
13 <160> NUMBER OF SEQ ID NOS: 8
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 3768
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: misc_feature
24 <222> LOCATION: 3395, 3437, and 3440
25 <223> OTHER INFORMATION: N=G,A,C or T
27 <400> SEQUENCE: 1
28 caggaactgg gccagctccg gtcccttccct tttggggctc tcactctgga gg atg ggg 58
29                                     Met Gly
30                                     1
32 tgg atg gga gaa aaa acc ggg aag atc ctg acg gag ttc ctc cag ttc 106
33 Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe
34      5              10              15
36 tat gaa gac cag tat ggc gtg gct ctc ttc aac agc atg cgc cat gag 154
37 Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu
38      20              25              30
40 att gag ggc acg ggg ctg ccg cag gcc cag ctg ctc tgg cgc aag gtg 202
41 Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val
42 35              40              45              50
44 cca ctg gac gag cgc atc gtc ttc tcg ggg aac ctc ttc cag cac cag 250
45 Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln
46      55              60              65
48 gag gac agc aag aag tgg aga aac cgc ttc agc ctc gtg ccc cac aac 298
49 Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro His Asn
50      70              75              80
52 tac ggg ctg gtg ctc tac gaa aac aaa gcg gcc tat gag cgg cag gtc 346
53 Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg Gln Val
54      85              90              95
58 cca cca cga gcc gtc atc aac agt gca ggc tac aaa atc ctc acg tcc 394
59 Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu Thr Ser
60 100              105              110
62 gtg gac caa tac ctg gag ctc att ggc aac tcc tta cca ggg acc acg 442
63 Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly Thr Thr

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64	115		120		125		130	
66	gca aag tgc ggc agt gcc ccc atc ctc aag tgc ccc aca cag ttc ccg	490						
67	Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln Phe Pro							
68			135		140		145	
70	ctc atc ctc tgg cat cct tat gcg cgt cac tac tac ttc tgc atg atg	538						
71	Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys Met Met							
72			150		155		160	
74	aca gaa gcc gag cag gac aag tgg cag gct gtg ctg cag gac tgc atc	586						
75	Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp Cys Ile							
76			165		170		175	
78	cgg cac tgc aac aat gga atc cct gag gac tcc aag gta gag ggc cct	634						
79	Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu Gly Pro							
80			180		185		190	
82	gcg ttc aca gat gcc atc cgc atg tac cga cag tcc aag gag ctg tac	682						
83	Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu Leu Tyr							
84	195		200		205		210	
86	ggc acc tgg gag atg ctg tgt ggg aac gag gtg cag atc ctg agc aac	730						
87	Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu Ser Asn							
88			215		220		225	
90	ctg gtg atg gag gag ctg ggc cct gag ctg aag gca gag ctc ggc ccg	778						
91	Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu Gly Pro							
92			230		235		240	
94	cgg ctg aag ggg aaa ccg cag gag cgg cag cgg cag tgg atc cag atc	826						
95	Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile Gln Ile							
96			245		250		255	
98	tgc gac gcc gtg tac cac atg gtg tac gag cag gcc aag gcg cgc ttc	874						
99	Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala Arg Phe							
100			260		265		270	
102	gag gag gtg ctg tcc aag gtg cag cag gtg cag ccg gcc atg cag gcc	922						
103	Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met Gln Ala							
104	275		280		285		290	
106	gtc atc cga act gac atg gac caa att atc acc tcc aag gag ctc ctt	970						
107	Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu Leu Leu							
108			295		300		305	
110	gcc agc aag atc cga gcc ttc atc ctc ccc aag gca gag gtg tgc gtg	1018						
111	Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val Cys Val							
112			310		315		320	
115	cgg aac cat gtc cag ccc tac atc cca tcc atc ctg gag gcc ctg atg	1066						
116	Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala Leu Met							
117			325		330		335	
119	gtc ccc acc agc cag ggc ttc act gag gtg cga gat gtc ttc ttc aag	1114						
120	Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe Phe Lys							
121			340		345		350	
123	gag gtc acg gac atg aac ctg aac gtc atc aac gag ggc ggc att gac	1162						
124	Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly Ile Asp							
125	355		360		365		370	
127	aag ctg ggc gag tac atg gag aag ctg tcc cgg ctg gcg tac cac ccc	1210						
128	Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr His Pro							
129			375		380		385	

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131 ctg aag atg cag agc tgc tat gag aag atg gag tcg ctg cga ctg gac 1258
132 Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg Leu Asp
133          390          395          400
135 ggg ctg cag cag cga ttt gat gtg tcc agc acg tcc gtg ttc aag cag 1306
136 Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe Lys Gln
137          405          410          415
139 cga gcc cag atc cac atg cgg gag caa atg gac aat gcc gtg tat acg 1354
140 Arg Ala Gln Ile His Met Arg Glu Gln Met Asp Asn Ala Val Tyr Thr
141          420          425          430
143 ttc gag acc ctc ctg cac gag gag ctg ggg aag ggg ccc acc aag gag 1402
144 Phe Glu Thr Leu Leu His Gln Glu Leu Gly Lys Gly Pro Thr Lys Glu
145 435          440          445          450
147 gag ctg tgc aag tcc atc cag cgg gtc ctg gag cgg gtg ctg aaa aaa 1450
148 Glu Leu Cys Lys Ser Ile Gln Arg Val Leu Glu Arg Val Leu Lys Lys
149          455          460          465
151 tac gac tac gac agc agc tct gtg cgg aag agg ttc ttc cgg gag gcg 1498
152 Tyr Asp Tyr Asp Ser Ser Ser Val Arg Lys Arg Phe Phe Arg Glu Ala
153          470          475          480
155 ctg ctg cag atc agc atc ccg ttc ctg ctc aag aag ctg gcc cct acc 1546
156 Leu Leu Gln Ile Ser Ile Pro Phe Leu Leu Lys Lys Leu Ala Pro Thr
157          485          490          495
159 tgc aag tcg gag ctg ccc cgg ttc cag gag ctg atc ttc gag gac ttt 1594
160 Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu Asp Phe
161          500          505          510
163 gcc agg ttc atc ctg gtg gaa aac acg tac gag gag gtg gtg ctg cag 1642
164 Ala Arg Phe Ile Leu Val Glu Asn Thr Tyr Glu Glu Val Val Leu Gln
165 515          520          525          530
167 acc gtc atg aag gac atc ctg cag gct gtg aag gag gcc gcg gtg cag 1690
168 Thr Val Met Lys Asp Ile Leu Gln Ala Val Lys Glu Ala Ala Val Gln
169          535          540          545
172 agg aag cac aac ctc tac cgg gac agc atg gtc atg cac aac agc gac 1738
173 Arg Lys His Asn Leu Tyr Arg Asp Ser Met Val Met His Asn Ser Asp
174          550          555          560
176 ccc aac ctg cac ctg ctg gcc gag ggc gcc ccc atc gac tgg ggc gag 1786
177 Pro Asn Leu His Leu Leu Ala Glu Gly Ala Pro Ile Asp Trp Gly Glu
178          565          570          575
180 gag tac agc aac agc ggc ggg ggc ggc agc ccc agc ccc agc acc ccg 1834
181 Glu Tyr Ser Asn Ser Gly Gly Gly Ser Pro Ser Pro Ser Thr Pro
182          580          585          590
184 gag tca gcc acc ctc tcg gaa aag cga cgg cgc gcc aag cag gtg gtc 1882
185 Glu Ser Ala Thr Leu Ser Glu Lys Arg Arg Arg Ala Lys Gln Val Val
186 595          600          605          610
188 tct gtg gtc cag gat gag gag gtg ggg ctg ccc ttt gag gct agc cct 1930
189 Ser Val Val Gln Asp Glu Glu Val Gly Leu Pro Phe Glu Ala Ser Pro
190          615          620          625
192 gag tca cca cca cct gcg tcc ccg gac ggt gtc act gag atc cga ggc 1978
193 Glu Ser Pro Pro Pro Ala Ser Pro Asp Gly Val Thr Glu Ile Arg Gly
194          630          635          640
196 ctg ctg gcc caa ggt ctg cgg cct gag agc ccc cca cca gcc ggc ccc 2026

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197 Leu Leu Ala Gln Gly Leu Arg Pro Glu Ser Pro Pro Pro Ala Gly Pro
198          645          650          655
200 ctg ctc aac ggg gcc ccc gct ggg gag agt ccc cag cct aag gcc gcc 2074
201 Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys Ala Ala
202          660          665          670
204 ccc gag gcc tcc tcg ccg cct gcc tca ccc ctc cag cat ctc ctg cct 2122
205 Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro Leu Gln His Leu Leu Pro
206 675          680          685          690
208 gga aag gct gtg gac ctt ggg ccc ccc aag ccc agc gac cag gag act 2170
209 Gly Lys Ala Val Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln Glu Thr
210          695          700          705
212 gga gag cag gtg tcc agc ccc agc agc cac ccc gcc ctc cac acc acc 2218
213 Gly Glu Gln Val Ser Ser Pro Ser Ser His Pro Ala Leu His Thr Thr
214          710          715          720
216 acc gag gac agt gca ggg gtg cag act gag ttc taggccagtg ggtccctgac 2271
217 Thr Glu Asp Ser Ala Gly Val Gln Thr Glu Phe
218          725          730
220 tgctgcacat ggcacaggcc gttcccttcc ggacccaggc aggcctcagct ctggggaggg 2331
222 caccctggtc tgtgccttgt ggggtggaggc ggggcagggc tgtgtggcac cgccaggagg 2391
224 cgggcccacc tgagtcactt tattgggttc agtcaacact ttcttgcctc ctgttttctc 2451
226 ttctgtggga tgatctcaga tgcaggggct ggttttgggg ttttctctgt tgtgccaagg 2511
228 gctggacact gctggggggc tggaaagccc ctcccttctc gtccttctgt ggccctccatc 2571
230 cctcatggg tgctgccatc cttcctggag agagggaggt gaaagctggt gtgagccag 2631
232 tgggttccc cccactcacc caggagctgg ctgggccagg accgggagag ggagcactgc 2691
234 tgcctcctg gccctgctcc ttccgcagtt aggggtggac cgagcctcgc tttccccact 2751
236 gttctggagg gaaggggaag gaggggtct tcaggctgga gccaggctgg ggggtgctgg 2811
238 tggagagatg agatttaggg ggtgcctcat ggggtgggca ggcttgggg gaaatgagaa 2871
240 aggccagaa cgtgcaggtc tgcggagggg aagtgtcctg agtgaaggag gggaccccat 2931
242 cctggggatg ctgggagtga gtgagtga tggctgagtg agggttatgg ggagcctgag 2991
244 gttttatggg cctgtgtatc ccttctctcc ggcccagcc tgcctccctc ctgcccgcct 3051
246 ggcccacagg tctcctctg gtccctgtcc ctctggtggt tggggatgga gcggcagcaa 3111
248 ggggtgtaat ggggctgggt tctgtcttct acaggccacc ccgaggtcct cagtggttgc 3171
250 ctggggagcc ggacggggct cctgaggggt acagggttgg tgggcccctc ctgaggggtct 3231
252 ggggtcaggc tttggcctct gctgcctctc agtcaccaag tcacctccct ctgaaaatcc 3291
254 agtcccttct ttgatgtcc ttgtgagtea ctctgggctt ggctgtcgtc cctcctcagc 3351
256 ttcttgttcc tgggacaagg gtcaagccag gatgggcccga ggcntgggat cccccacccc 3411
258 aggacccac agggcccctc cctgntgnt ttgcgggggg cagggcagaa atggactcct 3471
260 tttgggtccc cgaggtggg tcccctccca gccctgcatc ctccgtgccc tagacctgct 3531
262 cccagagga ggggccttga cccacaggaa gtgtggtggc gcctggcaat cagggacccc 3591
264 cagctgccgc agccctggtt tttggcgcat ctttccctc ttgtcccgaa gatttgcgcc 3651
266 tttagtgcct tttgaggggt tcccatcatc cctcctgat attgtattga aaatattatg 3711
268 cacactgttc atgcttttac taatcaataa acgctttatt taaaaaaaaa aaaaaaa 3768
271 <210> SEQ ID NO: 2
272 <211> LENGTH: 733
273 <212> TYPE: PRT
274 <213> ORGANISM: Homo sapiens
276 <400> SEQUENCE: 2
277 Met Gly Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu
278 1 5 10 15

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```

280 Gln Phe Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg
281          20          25          30
283 His Glu Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg
284          35          40          45
286 Lys Val Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln
287          50          55          60
289 His Gln Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro
290          65          70          75          80
292 His Asn Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg
293          85          90          95
295 Gln Val Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu
296          100         105         110
298 Thr Ser Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly
299          115         120         125
301 Thr Thr Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln
302          130         135         140
304 Phe Pro Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys
305          145         150         155         160
307 Met Met Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp
308          165         170         175
310 Cys Ile Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu
311          180         185         190
313 Gly Pro Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu
314          195         200         205
316 Leu Tyr Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu
317          210         215         220
319 Ser Asn Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu
320          225         230         235         240
322 Gly Pro Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile
323          245         250         255
325 Gln Ile Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala
326          260         265         270
328 Arg Phe Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met
329          275         280         285
331 Gln Ala Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu
332          290         295         300
334 Leu Leu Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val
335          305         310         315         320
337 Cys Val Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala
338          325         330         335
340 Leu Met Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe
341          340         345         350
343 Phe Lys Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly
344          355         360         365
346 Ile Asp Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr
347          370         375         380
349 His Pro Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg
350          385         390         395         400
352 Leu Asp Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 3395,3437,3440